

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/723, 003A  
Source: IFW16  
Date Processed by STIC: 01/25/2007

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/25/2007

PATENT APPLICATION: US/10/723,003A

TIME: 14:46:02

Input Set : A:\47630301.txt

Output Set: N:\CRF4\01252007\J723003A.raw

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4 <110> APPLICANT: MA, Jing
5      GUO, Yajun
7 <120> TITLE OF INVENTION: PREPARATION AND APPLICATION OF
8      ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
10 <130> FILE REFERENCE: 047630-0301
12 <140> CURRENT APPLICATION NUMBER: US 10/723,003A
13 <141> CURRENT FILING DATE: 2003-11-26
15 <150> PRIOR APPLICATION NUMBER: CN 2003101199300
16 <151> PRIOR FILING DATE: 2003-11-25
18 <150> PRIOR APPLICATION NUMBER: CN 031292909
19 <151> PRIOR FILING DATE: 2003-06-13
21 <160> NUMBER OF SEQ ID NOS: 70
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 546
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
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32 agctcgggac tcagtgggac ccaggactgc tccttccaac acagcccat ctcctccgac 120
33 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
34 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggtggt cctggcacag 240
35 cgctggatgg agcggctcaa gactgtcgct ggggtccaaga tgcaaggctt gctggagcgc 300
36 gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agccccccc cagctgtctt 360
37 cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctggtggcg 420
38 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
39 gactcctcaa cctgcccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
40 gccccg                                     546
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 182
44 <212> TYPE: PRT
45 <213> ORGANISM: Homo sapiens
47 <400> SEQUENCE: 2
48 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
49 1          5          10          15
50 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
51 20          25          30
52 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
53 35          40          45
54 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
55 50          55          60
56 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
57 65          70          75          80

```

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58 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
59           85           90           95
60 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
61           100          105          110
62 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
63           115          120          125
64 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
65           130          135          140
66 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
67 145           150          155          160
68 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
69           165          170          175
70 Thr Ala Pro Thr Ala Pro
71           180
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 1242
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Synthetic Construct
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84 agctcgggac tcagtgggac ccaggactgc tccttccaac acagcccatc ctctccgac 120
85 ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
86 gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
87 cgctggatgg agcgggtcaa gactgtcgct ggggtccaaga tgcaaggctt gctggagcgc 300
88 gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
89 cgcttcgtcc agaccaacat ctccgcctc ctgcaggaga cctccgagca gctgggtggc 420
90 ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
91 gactcctcaa ccctgccacc cccatggagt ccccgccccc tggaggccac agccccgaca 540
92 gccccggagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
93 ctcttggggg gaccgtcagt ctctctcttc cccccaaaac ccaaggacac cctcatgata 660
94 tcccggaccc ctgaggtcac atgcggtggtg gtggacgtga gccacgaaga cctgaggtc 720
95 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
96 gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
97 ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
98 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
99 tcccgggatg agctgaccaa gaaccaggtc agcctgacct gctggtcaa aggtttctat 1020
100 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
101 acgcctcccg tctggactc cgacggctcc ttcttctct acagcaagct caccgtggac 1140
102 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
103 aaccactaca cgcagaagag cctctccctg tctcccggta aa 1242
105 <210> SEQ ID NO: 4
106 <211> LENGTH: 414
107 <212> TYPE: PRT
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Synthetic Construct
113 <400> SEQUENCE: 4

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114 Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
115 1 5 10 15
116 Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
117 20 25 30
118 Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
119 35 40 45
120 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
121 50 55 60
122 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
123 65 70 75 80
124 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
125 85 90 95
126 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
127 100 105 110
128 Phe Gln Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
129 115 120 125
130 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
131 130 135 140
132 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
133 145 150 155 160
134 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
135 165 170 175
136 Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
137 180 185 190
138 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
139 195 200 205
140 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
141 210 215 220
142 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
143 225 230 235 240
144 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
145 245 250 255
146 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
147 260 265 270
148 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
149 275 280 285
150 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
151 290 295 300
152 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
153 305 310 315 320
154 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
155 325 330 335
156 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
157 340 345 350
158 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
159 355 360 365
160 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
161 370 375 380
162 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His

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163 385          390          395          400
164 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
165          405          410
168 <210> SEQ ID NO: 5
169 <211> LENGTH: 45
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Synthetic Construct
176 <400> SEQUENCE: 5
177 ggcgggtggag gctctggtgg aggcgggttca ggaggcgggtg gatct 45
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 15
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Synthetic Construct
187 <400> SEQUENCE: 6
188 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
189 1          5          10          15
192 <210> SEQ ID NO: 7
193 <211> LENGTH: 426
194 <212> TYPE: DNA
195 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 7
198 atcgccgccca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcagg 60
199 gtccactctg aggtccagct gcagcagctc ggacctgagc tggtaaagcc tggggcttca 120
200 gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcaactgggtg 180
201 aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
202 actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
203 acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
204 tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgctc 420
205 tcctca 426
207 <210> SEQ ID NO: 8
208 <211> LENGTH: 138
209 <212> TYPE: PRT
210 <213> ORGANISM: Mus musculus
212 <400> SEQUENCE: 8
213 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
214 1          5          10          15
215 Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
216          20          25          30
217 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
218          35          40          45
219 Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
220          50          55          60
221 Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
222 65          70          75          80
223 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser

```

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```

224      85      90      95
225 Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
226      100      105      110
227 Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
228      115      120      125
229 Gly Ala Gly Thr Thr Val Thr Val Ser Ser
230      130      135
233 <210> SEQ ID NO: 9
234 <211> LENGTH: 465
235 <212> TYPE: DNA
236 <213> ORGANISM: Mus musculus
238 <400> SEQUENCE: 9
239 atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc 60
240 gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctgggtacc 120
241 tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag 180
242 gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaata gaagaactac 240
243 ttggcctggg accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
244 actaggggaat ctgggtgtccc tgatcgcttc acagggcagtg gatctggggac agattttact 360
245 ctaccatca gcagtgtaca agctgaagac ctgggcagttt attactgtca tcaatatctc 420
246 tcctcataca cgctcggagg ggggaccaag ctggaaaataa agcgg 465
248 <210> SEQ ID NO: 10
249 <211> LENGTH: 133
250 <212> TYPE: PRT
251 <213> ORGANISM: Mus musculus
253 <400> SEQUENCE: 10
254 Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
255 1 5 10 15
256 Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
257 20 25 30
258 Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
259 35 40 45
260 Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
261 50 55 60
262 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
263 65 70 75 80
264 Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
265 85 90 95
266 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
267 100 105 110
268 Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
269 115 120 125
270 Leu Glu Ile Lys Arg
271 130
274 <210> SEQ ID NO: 11
275 <211> LENGTH: 2021
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Synthetic Construct

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**VERIFICATION SUMMARY**

DATE: 01/25/2007

PATENT APPLICATION: US/10/723,003A

TIME: 14:46:03

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Output Set: N:\CRF4\01252007\J723003A.raw